

0500
#4
ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/714,767

DATE: 12/01/2000

TIME: 13:32:14

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\12012000\I714767.raw

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4 <110> APPLICANT: Bidney, Dennis
5   Duvick, Jon
6   Hendrick, Carol
7   Hu, Xu
8   Lu, Guihua
9   Crasta, Oswald
12 <120> TITLE OF INVENTION: Sunflower RhoGAP, LOX, ADH and SCIP -
13   Polynucleotides and Methods of Use
16 <130> FILE REFERENCE: 35718/201902
C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/714,767
C--> 18 <141> CURRENT FILING DATE: 2000-11-16
18 <150> PRIOR APPLICATION NUMBER: US 60/166,128
19 <151> PRIOR FILING DATE: 1999-11-18
21 <150> PRIOR APPLICATION NUMBER: US 60/201,837
22 <151> PRIOR FILING DATE: 2000-05-03
24 <160> NUMBER OF SEQ ID NOS: 10
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 824
30 <212> TYPE: DNA
31 <213> ORGANISM: Helianthus annuus
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (0)...(0)
36 <223> OTHER INFORMATION: rhoGAP
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (35)...(637)
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42 ttccggcagca gtcacaaatcc aatcttcaat cacc atg gct gaa gaa caa ctg ccg      55
43                                     Met Ala Glu Glu Gln Leu Pro
44                                     1          5
46 cct gat caa att aaa ctg att cac aag ctt aat ttg ttc aaa atc aaa      103
47 Pro Asp Gln Ile Lys Leu Ile His Lys Leu Asn Leu Phe Lys Ile Lys
48   10          15          20
50 ggc aga gat aaa cac aat cgc aaa atc tta cga att gtc gga aaa aac      151
51 Gly Arg Asp Lys His Asn Arg Lys Ile Leu Arg Ile Val Gly Lys Asn
52   25          30          35
54 ttt cca gct aag agt ttg acc gtt gac ctg ttg aaa aaa tat cta gaa      199
55 Phe Pro Ala Lys Ser Leu Thr Val Asp Leu Leu Lys Lys Tyr Leu Glu
56   40          45          50          55
58 gtg aaa att ttc ccc aaa ctt gaa cga ccg ttt gtg gtg gtt tac gtt      247
59 Val Lys Ile Phe Pro Lys Leu Glu Arg Pro Phe Val Val Val Tyr Val
60   60          65          70
62 cac act gat gtt cag aag agc gag aat ttc cct gga ata tcc gtt ctg      295
63 His Thr Asp Val Gln Lys Ser Glu Asn Phe Pro Gly Ile Ser Val Leu
64   75          80          85
66 cgg tca gtt tac gac gcg att ccg atg acc gtg aaa caa tat ctt gag      343

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67 Arg Ser Val Tyr Asp Ala Ile Pro Met Thr Val Lys Gln Tyr Leu Gln
68          90          95          100
70 gcg gtt tac ttt gtt cat ccg gat ctg cag tcc aga att ttt ctg gct      391
71 Ala Val Tyr Phe Val His Pro Asp Leu Gln Ser Arg Ile Phe Leu Ala
72      105          110          115
74 aca ttt ggc cgg ctt atc ttc acc gga ggg tta tat gca aag ctg aga      439
75 Ihr Phe Gly Arg Leu Ile Phe Thr Gly Gly Leu Tyr Ala Lys Leu Arg
76 120          125          130          135
78 ttt gtg agt cga ttg gcg tat ctg tgg gaa cat gtg aaa agg aac gag      487
79 Phe Val Ser Arg Leu Ala Tyr Leu Trp Glu His Val Lys Arg Asn Glu
80          140          145          150
82 atc gag atc cca gag ttt gtc tac gat cat gat gag gat ctg gag tac      535
83 Ile Glu Ile Pro Glu Phe Val Tyr Asp His Asp Glu Asp Leu Glu Tyr
84          155          160          165
86 cgt ccg atg atg gat tac ggg ata gag agt gac cac gct aga gtt tat      583
87 Arg Pro Met Met Asp Tyr Gly Ile Glu Ser Asp His Ala Arg Val Tyr
88      170          175          180
90 gga gcg ccc gcg gtt gat tcc tct gtg gcg gct tat tcc atg agg tgt      631
91 Gly Ala Pro Ala Val Asp Ser Ser Val Ala Ala Tyr Ser Met Arg Cys
92      185          190          195
94 atc tca taggggaaat agttgttttt tcttttgttt ttgaaaatag gtgctaaaag      687
95 Ile Ser
96 200
98 aagtgcaata tatagtatatt agcaatatatt cgggtgttgt agtatgttga taacgggctt      747
99 ttcttataac attcattggt ctagttttct ttgtataaaa ttatttgata aattctttgt      807
100 aaaaaaaaaa aaaaaaa
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 201
104 <212> TYPE: PRT
105 <213> ORGANISM: Helianthus annuus
107 <400> SEQUENCE: 2
108 Met Ala Glu Glu Gln Leu Pro Pro Asp Gln Ile Lys Leu Ile His Lys
109 1          5          10          15
110 Leu Asn Leu Phe Lys Ile Lys Gly Arg Asp Lys His Asn Arg Lys Ile
111      20          25          30
112 Leu Arg Ile Val Gly Lys Asn Phe Pro Ala Lys Ser Leu Thr Val Asp
113      35          40          45
114 Leu Leu Lys Lys Tyr Leu Glu Val Lys Ile Phe Pro Lys Leu Glu Arg
115      50          55          60
116 Pro Phe Val Val Val Tyr Val His Thr Asp Val Gln Lys Ser Glu Asn
117 65          70          75          80
118 Phe Pro Gly Ile Ser Val Leu Arg Ser Val Tyr Asp Ala Ile Pro Met
119      85          90          95
120 Thr Val Lys Gln Tyr Leu Glu Ala Val Tyr Phe Val His Pro Asp Leu
121      100          105          110
122 Gln Ser Arg Ile Phe Leu Ala Thr Phe Gly Arg Leu Ile Phe Thr Gly
123      115          120          125
124 Gly Leu Tyr Ala Lys Leu Arg Phe Val Ser Arg Leu Ala Tyr Leu Trp
125      130          135          140

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126 Glu His Val Lys Arg Asn Glu Ile Glu Ile Pro Glu Phe Val Tyr Asp
127 145 150 155 160
128 His Asp Glu Asp Leu Glu Tyr Arg Pro Met Met Asp Tyr Gly Ile Glu
129 165 170 175
130 Ser Asp His Ala Arg Val Tyr Gly Ala Pro Ala Val Asp Ser Ser Val
131 180 185 190
132 Ala Ala Tyr Ser Met Arg Cys Ile Ser
133 195 200
135 <210> SEQ ID NO: 3
136 <211> LENGTH: 2943
137 <212> TYPE: DNA
138 <213> ORGANISM: Helianthus annuus
140 <220> FEATURE:
141 <221> NAME/KEY: misc_feature
142 <222> LOCATION: (0)...(0)
143 <223> OTHER INFORMATION: lox cDNA
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (18)...(2720)
148 <400> SEQUENCE: 3
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150 Met Leu Asn Ser Gln Ile Asn His Ser His Pro
151 1 5 10
153 ctt aac aac cta cta cca atc cgc aaa gcc ttt gtc cat ggt gac acc 98
154 Leu Asn Asn Leu Leu Pro Ile Arg Lys Ala Phe Val His Gly Asp Thr
155 15 20 25
157 act aac cat tcc tcc tcc aac gcc tac tcc ccc gcc aac ctt cgc caa 146
158 Thr Asn His Ser Ser Ser Asn Ala Tyr Ser Pro Ala Asn Leu Arg Gln
159 30 35 40
161 cac gcg tcc acc aag aaa tcc aat gct acc cgt gca cga tcc acc tca 194
162 His Ala Ser Thr Lys Lys Ser Asn Ala Thr Arg Ala Arg Ser Thr Ser
163 45 50 55
165 act gcg ggt aac att aaa gcc ata tca atc ccc ttt ctt acc aag gag 242
166 Thr Ala Gly Asn Ile Lys Ala Ile Ser Ile Pro Phe Leu Thr Lys Glu
167 60 65 70 75
169 acc acc gtc aag tgt gtc atc acc gtc caa cca acc att agt tcc gcc 290
170 Thr Thr Val Lys Cys Val Ile Thr Val Gln Pro Thr Ile Ser Ser Ala
171 80 85 90
173 att gct ggt gta gcc gtt ggt ggt att gtt gat ggt gtt tct aat ctt 338
174 Ile Ala Gly Val Gly Val Gly Gly Ile Val Asp Gly Val Ser Asn Leu
175 95 100 105
177 cta ggg ttg tca ttt ttg ttg gag ctc gtt tca aat gac ctc gat tca 386
178 Leu Gly Leu Ser Phe Leu Leu Glu Leu Val Ser Asn Asp Leu Asp Ser
179 110 115 120
181 aaa gga aac caa aag aca gta aag gct tat gca aga tac aac gca ctg 434
182 Lys Gly Asn Gln Lys Thr Val Lys Ala Tyr Ala Arg Tyr Asn Ala Leu
183 125 130 135
185 gat ttg gac att agc gtg tac aca tac aaa tgc gac ttc gac gtc cct 482
186 Asp Leu Asp Ile Ser Val Tyr Thr Tyr Lys Cys Asp Phe Asp Val Pro
187 140 145 150 155

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189	gaa gat ttt ggg gag ata gga gct gtg ttg gta gaa aat gag tat agc	530
190	Glu Asp Phe Gly Glu Ile Gly Ala Val Leu Val Glu Asn Glu Tyr Ser	
191	160 165 170	
193	aag aag atg ttt ttc aag aac att gtt ctt aac aac ggt gtt acc ttc	578
194	Lys Lys Met Phe Phe Lys Asn Ile Val Leu Asn Asn Gly Val Thr Phe	
195	175 180 185	
197	aca tgc gag tca tgg gtt cac tcc aaa tac gat aac cct gag aaa aga	626
198	Thr Cys Glu Ser Trp Val His Ser Lys Tyr Asp Asn Pro Glu Lys Arg	
199	190 195 200	
201	ata ttt ttc acc gac aag tgc tat cta ccg ttg gaa acg ccg acg gca	674
202	Ile Phe Phe Thr Asp Lys Ser Tyr Leu Pro Leu Glu Thr Pro Thr Ala	
203	205 210 215	
205	ctg aag ccg tta cga gag aaa gat atg gaa tgc ctt cga gga aac ggc	722
206	Leu Lys Pro Leu Arg Glu Lys Asp Met Glu Ser Leu Arg Gly Asn Gly	
207	220 225 230 235	
209	gaa gga gaa cgt aaa tca ttc gag ccg ata tat gat tat gat gtg tac	770
210	Glu Gly Glu Arg Lys Ser Phe Glu Arg Ile Tyr Asp Tyr Asp Val Tyr	
211	240 245 250	
213	aac gat ctc gga gat ccg gat gga agc tta gat cta gca ccg ccg gtg	818
214	Asn Asp Leu Gly Asp Pro Asp Gly Ser Leu Asp Leu Ala Arg Pro Val	
215	255 260 265	
217	ctc ggt ggc gag aca cat ccg tac cct agc ccg tgc cgt act ggt cgc	866
218	Leu Gly Gly Glu Thr His Pro Tyr Pro Arg Arg Cys Arg Thr Gly Arg	
219	270 275 280	
221	aaa atg tcc tct aaa gat ccg tta aca gaa agc aga act acg ctc cct	914
222	Lys Met Ser Ser Lys Asp Pro Leu Thr Glu Ser Arg Thr Thr Leu Pro	
223	285 290 295	
225	ttt tat gta cct gcg gat gaa gat ttt tca gag ata aag agt gtg aac	962
226	Phe Tyr Val Pro Ala Asp Glu Asp Phe Ser Glu Ile Lys Ser Val Asn	
227	300 305 310 315	
229	ttt gga gca aaa act tta tac tct gtg ctt cat gga gtt gta cca atg	1010
230	Phe Gly Ala Lys Thr Leu Tyr Ser Val Leu His Gly Val Val Pro Met	
231	320 325 330	
233	cta gac tca att gta aca gac aaa gac aag ggg ttt cca tta ttc aca	1058
234	Leu Asp Ser Ile Val Thr Asp Lys Asp Lys Gly Phe Pro Leu Phe Thr	
235	335 340 345	
237	tcc ata gat ttg ctt tat aat gaa ggt gtt aat gtt cct tct cct gac	1106
238	Ser Ile Asp Leu Leu Tyr Asn Glu Gly Val Asn Val Pro Ser Pro Asp	
239	350 355 360	
241	aat gga att cta agt gct tta cct aga ctt gtc aaa ggg gct act gat	1154
242	Asn Gly Ile Leu Ser Ala Leu Pro Arg Leu Val Lys Gly Ala Thr Asp	
243	365 370 375	
245	gcc gca aat acc gtt atc aag ttc gag acc ccc gaa acc att gat aga	1202
246	Ala Ala Asn Thr Val Ile Lys Phe Glu Thr Pro Glu Thr Ile Asp Arg	
247	380 385 390 395	
249	gac gca ttc tca tgg ttc cgt gat gaa gag ttc tgc ccg caa atg ctt	1250
250	Asp Ala Phe Ser Trp Phe Arg Asp Glu Glu Phe Cys Arg Gln Met Leu	
251	400 405 410	
253	gcc ggt att aat cct tgt cgc ata caa ttg gtt acg gaa tgg cca ttg	1298

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254	Ala	Gly	Ile	Asn	Pro	Cys	Arg	Ile	Gln	Leu	Val	Thr	Glu	Trp	Pro	Leu	
255				415					420					425			
257	atg	agt	aaa	ctg	gac	cct	gaa	atc	tat	gga	cca	gct	gag	tca	gca	att	1346
258	Met	Ser	Lys	Leu	Asp	Pro	Glu	Ile	Tyr	Gly	Pro	Ala	Glu	Ser	Ala	Ile	
259			430					435					440				
261	aca	aag	gag	att	gta	gag	gaa	gag	att	aaa	ggt	ttc	atg	act	ctt	gag	1394
262	Thr	Lys	Glu	Ile	Val	Glu	Glu	Glu	Ile	Lys	Gly	Phe	Met	Thr	Leu	Glu	
263			445					450					455				
265	gag	gct	tta	gca	caa	aag	aag	ctg	ttt	atg	ctg	gat	tat	cat	gat	ctg	1442
266	Glu	Ala	Leu	Ala	Gln	Lys	Lys	Leu	Phe	Met	Leu	Asp	Tyr	His	Asp	Leu	
267	460					465					470				475		
269	ctc	ttg	cct	tat	gtt	aac	aaa	acg	gag	gct	gaa	ggg	aga	act	ttg	tat	1490
270	Leu	Leu	Pro	Tyr	Val	Asn	Lys	Thr	Glu	Ala	Glu	Gly	Arg	Thr	Leu	Tyr	
271				480						485					490		
273	ggt	tca	aga	act	tta	atg	ttc	ctt	act	cct	gct	gga	aca	tta	agg	cca	1538
274	Gly	Ser	Arg	Thr	Leu	Met	Phe	Leu	Thr	Pro	Ala	Gly	Thr	Leu	Arg	Pro	
275				495					500					505			
277	cta	gcc	att	gag	ctg	act	cgc	cca	cca	att	gat	ggg	aaa	cca	cag	tgg	1586
278	Leu	Ala	Ile	Glu	Leu	Thr	Arg	Pro	Pro	Ile	Asp	Gly	Lys	Pro	Gln	Trp	
279			510					515					520				
281	aaa	cat	gtt	tac	aca	ccc	gct	tgg	gat	gct	aca	ggt	gca	tgg	ctt	tgg	1634
282	Lys	His	Val	Tyr	Thr	Pro	Ala	Trp	Asp	Ala	Thr	Gly	Ala	Trp	Leu	Trp	
283			525				530					535					
285	aag	cta	gcc	aag	gct	cat	gtc	ctt	gcc	cat	gat	tct	agc	tat	cac	caa	1682
286	Lys	Leu	Ala	Lys	Ala	His	Val	Leu	Ala	His	Asp	Ser	Ser	Tyr	His	Gln	
287	540					545					550				555		
289	ctt	gtt	agc	cat	tgg	cta	aga	aca	cat	tgt	gct	acc	gaa	cct	tac	att	1730
290	Leu	Val	Ser	His	Trp	Leu	Arg	Thr	His	Cys	Ala	Thr	Glu	Pro	Tyr	Ile	
291				560					565					570			
293	att	gct	acc	aat	cgc	caa	ctc	agt	caa	atg	cat	cca	att	cga	cga	ttt	1778
294	Ile	Ala	Thr	Asn	Arg	Gln	Leu	Ser	Gln	Met	His	Pro	Ile	Arg	Arg	Phe	
295			575						580					585			
297	cta	ctc	cct	cac	ttt	cgt	tac	act	atg	caa	att	aat	tct	cta	gct	aga	1826
298	Leu	Leu	Pro	His	Phe	Arg	Tyr	Thr	Met	Gln	Ile	Asn	Ser	Leu	Ala	Arg	
299			590					595					600				
301	ctt	tta	ctc	gtc	aat	gcc	atg	ggt	atc	ata	gag	tca	aca	ttt	tct	cct	1874
302	Leu	Leu	Leu	Val	Asn	Ala	Met	Gly	Ile	Ile	Glu	Ser	Thr	Phe	Ser	Pro	
303		605				610						615					
305	gga	aga	tat	tgt	atg	caa	att	tcc	tct	gat	gca	tat	gat	cag	caa	tgg	1922
306	Gly	Arg	Tyr	Cys	Met	Gln	Ile	Ser	Ser	Asp	Ala	Tyr	Asp	Gln	Gln	Trp	
307	620					625					630				635		
309	cgt	ttt	gat	cat	gaa	gcg	ctt	ccg	gcc	gac	cta	att	agc	agg	ggt	atg	1970
310	Arg	Phe	Asp	His	Glu	Ala	Leu	Pro	Ala	Asp	Leu	Ile	Ser	Arg	Gly	Met	
311				640					645					650			
313	gcg	gtt	gaa	gat	cca	acc	gca	cca	tat	ggt	gta	aaa	cta	aca	atc	gag	2018
314	Ala	Val	Glu	Asp	Pro	Thr	Ala	Pro	Tyr	Gly	Val	Lys	Leu	Thr	Ile	Glu	
315			655						660					665			
317	gat	tac	cca	tat	gca	aat	gat	ggt	tta	ctc	att	tat	gat	acc	att	aaa	2066
318	Asp	Tyr	Pro	Tyr	Ala	Asn	Asp	Gly	Leu	Leu	Ile	Tyr	Asp	Thr	Ile	Lys	

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L:18 M:270 C: Current Application Number differs, Replaced Current Application No
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date